

SEQUENCE LISTING

<110> Lockridge, Oksana
Watkins, Jeffry D.

<120> Butyrylcholinesterase Variants and
Methods of Use

<130> P-IX 4143

<140> US 09/748,739

<141> 2000-12-26

<160> 31

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1967

<212> DNA

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<221> CDS

<222> (86)...(1891)

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cgcgcgacaga tcttcggaag ccacc atg gat agc aaa gtc aca atc ata tgc 112
Met Asp Ser Lys Val Thr Ile Ile Cys

1

5

atc aga ttt ctc ttt tgg ttt ctt ttg ctc tgc atg ctt att ggg aag 160
Ile Arg Phe Leu Phe Trp Phe Leu Leu Leu Cys Met Leu Ile Gly Lys
10 15 20 25

tca cat act gaa gat gac atc ata att gca aca aag aat gga aaa gtc 208
Ser His Thr Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val
30 35 40

aga ggg atg aac ttg aca gtt ttt ggt ggc acg gta aca gcc ttt ctt 256
Arg Gly Met Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu
45 50 55

gga att ccc tat gca cag cca cct ctt ggt aga ctt cga ttc aaa aag 304
Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys
60 65 70

cca cag tct ctg acc aag tgg tct gat att tgg aat gcc aca aaa tat 352
Pro Gln Ser Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr

75	80	85	
gca aat tct tgc tgt cag aac ata gat caa agt ttt cca ggc ttc cat			400
Ala Asn Ser Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His			
90	95	100	105
gga tca gag atg tgg aac cca aac act gac ctc agt gaa gac tgt tta			448
Gly Ser Glu Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu			
	110	115	120
tat cta aat gta tgg att cca gca cct aaa cca aaa aat gcc act gta			496
Tyr Leu Asn Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val			
	125	130	135
ttg ata tgg att tat ggt ggt ggt ttt caa act gga aca tca tct tta			544
Leu Ile Trp Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu			
	140	145	150
cat gtt tat gat ggc aag ttt ctg gct cgg gtt gaa aga gtt att gta			592
His Val Tyr Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val			
	155	160	165
gtg tca atg aac tat agg gtg ggt gcc cta gga ttc tta gct ttg cca			640
Val Ser Met Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro			
170	175	180	185
gga aat cct gag gct cca ggg aac atg ggt tta ttt gat caa cag ttg			688
Gly Asn Pro Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu			
	190	195	200
gct ctt cag tgg gtt caa aaa aat ata gca gcc ttt ggt gga aat cct			736
Ala Leu Gln Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro			
	205	210	215
aaa agt gta act ctc ttt gga gaa agt gca gga gca gct tca gtt agc			784
Lys Ser Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser			
	220	225	230
ctg cat ttg ctt tct cct gga agc cat tca ttg ttc acc aga gcc att			832
Leu His Leu Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile			
	235	240	245
ctg caa agt ggt tcc ttt aat gct cct tgg gcg gta aca tct ctt tat			880
Leu Gln Ser Gly Ser Phe Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr			
250	255	260	265
gaa gct agg aac aga acg ttg aac tta gct aaa ttg act ggt tgc tct			928
Glu Ala Arg Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser			
	270	275	280
aga gag aat gag act gaa ata atc aag tgt ctt aga aat aaa gat ccc			976
Arg Glu Asn Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro			
	285	290	295

caa gaa att ctt ctg aat gaa gca ttt gtt gtc ccc tat ggg act cct	1024
Gln Glu Ile Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro	
300 305 310	
ttg tca gta aac ttt ggt ccg acc gtg gat ggt gat ttt ctc act gac	1072
Leu Ser Val Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp	
315 320 325	
atg cca gac ata tta ctt gaa ctt gga caa ttt aaa aaa acc cag att	1120
Met Pro Asp Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile	
330 335 340 345	
ttg gtg ggt gtt aat aaa gat gaa ggg aca tgg ttt tta gtc tat ggt	1168
Leu Val Gly Val Asn Lys Asp Glu Gly Thr Trp Phe Leu Val Tyr Gly	
350 355 360	
gct cct ggc ttc agc aaa gat aac aat agt atc ata act aga aaa gaa	1216
Ala Pro Gly Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu	
365 370 375	
ttt cag gaa ggt tta aaa ata ttt ttt cca gga gtg agt gag ttt gga	1264
Phe Gln Glu Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly	
380 385 390	
aag gaa tcc atc ctt ttt cat tac aca gac tgg gta gat gat cag aga	1312
Lys Glu Ser Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg	
395 400 405	
cct gaa aac tac cgt gag gcc ttg ggt gat gtt gtt ggg gat tat aat	1360
Pro Glu Asn Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn	
410 415 420 425	
ttc ata tgc cct gcc ttg gag ttc acc aag aag ttc tca gaa tgg gga	1408
Phe Ile Cys Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly	
430 435 440	
aat aat gcc ttt ttc tac tat ttt gaa cac cga tcc tcc aaa ctt ccg	1456
Asn Asn Ala Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro	
445 450 455	
tgg cca gaa tgg atg gga gtg atg cat ggc tat gaa att gaa ttt gtc	1504
Trp Pro Glu Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val	
460 465 470	
ttt ggt tta cct ctg gaa aga aga gat aat tac aca aaa gcc gag gaa	1552
Phe Gly Leu Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu	
475 480 485	
att ttg agt aga tcc ata gtg aaa cgg tgg gca aat ttt gca aaa tat	1600
Ile Leu Ser Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr	
490 495 500 505	

ggg aat cca aat gag act cag aac aat agc aca agc tgg cct gtc ttc	1648
Gly Asn Pro Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe	
510 515 520	

aaa agc act gaa caa aaa tat cta acc ttg aat aca gag tca aca aga	1696
Lys Ser Thr Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg	
525 530 535	

ata atg acg aaa cta cgt gct caa caa tgt cga ttc tgg aca tca ttt	1744
Ile Met Thr Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe	
540 545 550	

ttt cca aaa gtc ttg gaa atg aca gga aat att gat gaa gca gaa tgg	1792
Phe Pro Lys Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp	
555 560 565	

gag tgg aaa gca gga ttc cat cgc tgg aac aat tac atg atg gac tgg	1840
Glu Trp Lys Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp	
570 575 580 585	

aaa aat caa ttt aac gat tac act agc aag aaa gaa agt tgt gtg ggt	1888
Lys Asn Gln Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly	
590 595 600	

ctc taattaatag atctgtcatg atgatcattg caattggatc catatatagg	1941
Leu	

gccctattct atagtgtcac ctaa	1967
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<211> 602

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 2

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Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met Asn Leu Thr Val	
35 40 45	
Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro Tyr Ala Gln Pro	
50 55 60	
Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser Leu Thr Lys Trp	
65 70 75 80	
Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser Cys Cys Gln Asn	
85 90 95	
Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu Met Trp Asn Pro	
100 105 110	

Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp	Ile	Pro
	115						120					125			
Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	Ile	Tyr	Gly	Gly
	130					135						140			
Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	Asp	Gly	Lys	Phe
145					150					155					160
Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	Asn	Tyr	Arg	Val
			165					170						175	
Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	Glu	Ala	Pro	Gly
		180						185					190		
Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	Trp	Val	Gln	Lys
	195					200						205			
Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	Thr	Leu	Phe	Gly
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Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	Leu	Ser	Pro	Gly
225					230					235					240
Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	Gly	Ser	Phe	Asn
				245					250					255	
Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	Asn	Arg	Thr	Leu
		260						265					270		
Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	Glu	Thr	Glu	Ile
	275						280					285			
Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	Leu	Leu	Asn	Glu
	290					295					300				
Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	Asn	Phe	Gly	Pro
305					310					315					320
Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	Ile	Leu	Leu	Glu
				325					330					335	
Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	Val	Asn	Lys	Asp
			340					345					350		
Glu	Gly	Thr	Trp	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	Phe	Ser	Lys	Asp
	355						360					365			
Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	Gly	Leu	Lys	Ile
	370					375					380				
Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	Ile	Leu	Phe	His
385					390					395					400
Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	Tyr	Arg	Glu	Ala
				405					410					415	
Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	Pro	Ala	Leu	Glu
		420					425						430		
Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	Phe	Phe	Tyr	Tyr
	435						440					445			
Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	Trp	Met	Gly	Val
	450					455					460				
Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	Pro	Leu	Glu	Arg
465					470					475					480
Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	Arg	Ser	Ile	Val
				485					490					495	
Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	Asn	Glu	Thr	Gln
		500						505					510		
Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	Glu	Gln	Lys	Tyr
	515						520					525			
Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	Lys	Leu	Arg	Ala

530		535		540
Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys Val Leu Glu Met				
545		550		555
Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys Ala Gly Phe His				
	565		570	
Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln Phe Asn Asp Tyr				
	580		585	590
Thr Ser Lys Lys Glu Ser Cys Val Gly Leu				
595		600		

<210> 3

<211> 2416

<212> DNA

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<221> CDS

<222> (214) ... (1935)

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gaaatcaata tgcataagcaa agtcacaatc atatgcatca gatttctctt ttggtttctt 180
ttgctctgca tgcttattgg gaagtcacat act gaa gat gac atc ata att gca 234
Glu Asp Asp Ile Ile Ile Ala
1 5

aca aag aat gga aaa gtc aga ggg atg aac ttg aca gtt ttt ggt ggc 282
Thr Lys Asn Gly Lys Val Arg Gly Met Asn Leu Thr Val Phe Gly Gly
10 15 20

acg gta aca gcc ttt ctt gga att ccc tat gca cag cca cct ctt ggt 330
Thr Val Thr Ala Phe Leu Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
25 30 35

aga ctt cga ttc aaa aag cca cag tct ctg acc aag tgg tct gat att 378
Arg Leu Arg Phe Lys Lys Pro Gln Ser Leu Thr Lys Trp Ser Asp Ile
40 45 50 55

tgg aat gcc aca aaa tat gca aat tct tgc tgt cag aac ata gat caa 426
Trp Asn Ala Thr Lys Tyr Ala Asn Ser Cys Cys Gln Asn Ile Asp Gln
60 65 70

agt ttt cca ggc ttc cat gga tca gag atg tgg aac cca aac act gac 474
Ser Phe Pro Gly Phe His Gly Ser Glu Met Trp Asn Pro Asn Thr Asp
75 80 85

ctc agt gaa gac tgt tta tat cta aat gta tgg att cca gca cct aaa 522
Leu Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ile Pro Ala Pro Lys
90 95 100

cca aaa aat gcc act gta ttg ata tgg att tat ggt ggt ggt ttt caa	570
Pro Lys Asn Ala Thr Val Leu Ile Trp Ile Tyr Gly Gly Gly Phe Gln	
105 110 115	
act gga aca tca tct tta cat gtt tat gat ggc aag ttt ctg gct cgg	618
Thr Gly Thr Ser Ser Leu His Val Tyr Asp Gly Lys Phe Leu Ala Arg	
120 125 130 135	
gtt gaa aga gtt att gta gtg tca atg aac tat agg gtg ggt gcc cta	666
Val Glu Arg Val Ile Val Val Ser Met Asn Tyr Arg Val Gly Ala Leu	
140 145 150	
gga ttc tta gct ttg cca gga aat cct gag gct cca ggg aac atg ggt	714
Gly Phe Leu Ala Leu Pro Gly Asn Pro Glu Ala Pro Gly Asn Met Gly	
155 160 165	
tta ttt gat caa cag ttg gct ctt cag tgg gtt caa aaa aat ata gca	762
Leu Phe Asp Gln Gln Leu Ala Leu Gln Trp Val Gln Lys Asn Ile Ala	
170 175 180	
gcc ttt ggt gga aat cct aaa agt gta act ctc ttt gga gaa agt gca	810
Ala Phe Gly Gly Asn Pro Lys Ser Val Thr Leu Phe Gly Glu Ser Ala	
185 190 195	
gga gca gct tca gtt agc ctg cat ttg ctt tct cct gga agc cat tca	858
Gly Ala Ala Ser Val Ser Leu His Leu Leu Ser Pro Gly Ser His Ser	
200 205 210 215	
ttg ttc acc aga gcc att ctg caa agt gga tcc ttt aat gct cct tgg	906
Leu Phe Thr Arg Ala Ile Leu Gln Ser Gly Ser Phe Asn Ala Pro Trp	
220 225 230	
gcg gta aca tct ctt tat gaa gct agg aac aga acg ttg aac tta gct	954
Ala Val Thr Ser Leu Tyr Glu Ala Arg Asn Arg Thr Leu Asn Leu Ala	
235 240 245	
aaa ttg act ggt tgc tct aga gag aat gag act gaa ata atc aag tgt	1002
Lys Leu Thr Gly Cys Ser Arg Glu Asn Glu Thr Glu Ile Ile Lys Cys	
250 255 260	
ctt aga aat aaa gat ccc caa gaa att ctt ctg aat gaa gca ttt gtt	1050
Leu Arg Asn Lys Asp Pro Gln Glu Ile Leu Leu Asn Glu Ala Phe Val	
265 270 275	
gtc ccc tat ggg act cct ttg ggt gta aac ttt ggt ccg acc gtg gat	1098
Val Pro Tyr Gly Thr Pro Leu Gly Val Asn Phe Gly Pro Thr Val Asp	
280 285 290 295	
ggg gat ttt ctc act gac atg cca gac ata tta ctt gaa ctt gga caa	1146
Gly Asp Phe Leu Thr Asp Met Pro Asp Ile Leu Leu Glu Leu Gly Gln	
300 305 310	

ttt aaa aaa acc cag att ttg gtg ggt gtt aat aaa gat gaa ggg aca	1194
Phe Lys Lys Thr Gln Ile Leu Val Gly Val Asn Lys Asp Glu Gly Thr	
315 320 325	
gct ttt tta gtc tat ggt gct cct ggc ttc agc aaa gat aac aat agt	1242
Ala Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp Asn Asn Ser	
330 335 340	
atc ata act aga aaa gaa ttt cag gaa ggt tta aaa ata ttt ttt cca	1290
Ile Ile Thr Arg Lys Glu Phe Gln Glu Gly Leu Lys Ile Phe Phe Pro	
345 350 355	
gga gtg agt gag ttt gga aag gaa tcc atc ctt ttt cat tac aca gac	1338
Gly Val Ser Glu Phe Gly Lys Glu Ser Ile Leu Phe His Tyr Thr Asp	
360 365 370 375	
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Trp Val Asp Asp Gln Arg Pro Glu Asn Tyr Arg Glu Ala Leu Gly Asp	
380 385 390	
gtt gtt ggg gat tat aat ttc ata tgc cct gcc ttg gag ttc acc aag	1434
Val Val Gly Asp Tyr Asn Phe Ile Cys Pro Ala Leu Glu Phe Thr Lys	
395 400 405	
aag ttc tca gaa tgg gga aat aat gcc ttt ttc tac tat ttt gaa cac	1482
Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe Phe Tyr Tyr Phe Glu His	
410 415 420	
cga tcc tcc aaa ctt ccg tgg cca gaa tgg atg gga gtg atg cat ggc	1530
Arg Ser Ser Lys Leu Pro Trp Pro Glu Trp Met Gly Val Met His Gly	
425 430 435	
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Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro Leu Glu Arg Arg Asp Asn	
440 445 450 455	
tac aca aaa gcc gag gaa att ttg agt aga tcc ata gtg aaa cgg tgg	1626
Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg Ser Ile Val Lys Arg Trp	
460 465 470	
gca aat ttt gca aaa tat ggg aat cca aat gag act cag aac aat agc	1674
Ala Asn Phe Ala Lys Tyr Gly Asn Pro Asn Glu Thr Gln Asn Asn Ser	
475 480 485	
aca agc tgg cct gtc ttc aaa agc act gaa caa aaa tat cta acc ttg	1722
Thr Ser Trp Pro Val Phe Lys Ser Thr Glu Gln Lys Tyr Leu Thr Leu	
490 495 500	
aat aca gag tca aca aga ata atg acg aaa cta cgt gct caa caa tgt	1770
Asn Thr Glu Ser Thr Arg Ile Met Thr Lys Leu Arg Ala Gln Gln Cys	
505 510 515	
cga ttc tgg aca tca ttt ttt cca aaa gtc ttg gaa atg aca gga aat	1818

Arg Phe Trp Thr Ser Phe Phe Pro Lys Val Leu Glu Met Thr Gly Asn
520 525 530 535

att gat gaa gca gaa tgg gag tgg aaa gca gga ttc cat cgc tgg aac 1866
Ile Asp Glu Ala Glu Trp Glu Trp Lys Ala Gly Phe His Arg Trp Asn
540 545 550

aat tac atg atg gac tgg aaa aat caa ttt aac gat tac act agc aag 1914
Asn Tyr Met Met Asp Trp Lys Asn Gln Phe Asn Asp Tyr Thr Ser Lys
555 560 565

aaa gaa agt tgt gtg ggt ctc taattaatag atttaccctt tatagaacat 1965
Lys Glu Ser Cys Val Gly Leu
570

attttccttt agatcaaggc aaaaatatca ggagcttttt tacacaccta ctaaaaaagt 2025
tattatgtag ctgaaacaaa aatgccagaa ggataatatt gattcctcac atctttaact 2085
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aatataaagt tctacagtta attatgtgca tattaaaaca atggcctggt tcaatttctt 2205
tctttcctta ataaatttaa gttttttccc cccaaaatta tcagtgtctt gcttttagtc 2265
acgtgtattt tcattaccac tcgtaaaaag gtatcttttt taaatgaatt aaatattgaa 2325
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<210> 4

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 4

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35 40 45
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser
50 55 60
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu
65 70 75 80
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn
85 90 95
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp
100 105 110
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr
115 120 125
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met
130 135 140
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro
145 150 155 160

Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Gly	Val	275	280	285
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	340	345	350
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	355	360	365
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	370	375	380
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	385	390	395
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala	405	410	415
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser	450	455	460
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	465	470	475
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr	485	490	495
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr	500	505	510
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys	515	520	525
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys	530	535	540
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	545	550	555
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu			565	570	

<210> 5
 <211> 2416
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human Butyrylcholinesterase variant

<221> CDS
 <222> (214)...(1935)

<400> 5
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 ccgaagtatt acatgatttt cactccttgc aaactttacc atctttgttg cagagaatcg 120
 gaaatcaata tgcatagcaa agtcacaatc atatgcatca gatttctctt ttggtttctt 180
 ttgctctgca tgcttattgg gaagtcacat act gaa gat gac atc ata att gca 234
 Glu Asp Asp Ile Ile Ile Ala
 1 5

aca aag aat gga aaa gtc aga ggg atg aac ttg aca gtt ttt ggt ggc 282
 Thr Lys Asn Gly Lys Val Arg Gly Met Asn Leu Thr Val Phe Gly Gly
 10 15 20

acg gta aca gcc ttt ctt gga att ccc tat gca cag cca cct ctt ggt 330
 Thr Val Thr Ala Phe Leu Gly Ile Pro Tyr Ala Gln Pro Pro Leu Gly
 25 30 35

aga ctt cga ttc aaa aag cca cag tct ctg acc aag tgg tct gat att 378
 Arg Leu Arg Phe Lys Lys Pro Gln Ser Leu Thr Lys Trp Ser Asp Ile
 40 45 50 55

tgg aat gcc aca aaa tat gca aat tct tgc tgt cag aac ata gat caa 426
 Trp Asn Ala Thr Lys Tyr Ala Asn Ser Cys Cys Gln Asn Ile Asp Gln
 60 65 70

agt ttt cca ggc ttc cat gga tca gag atg tgg aac cca aac act gac 474
 Ser Phe Pro Gly Phe His Gly Ser Glu Met Trp Asn Pro Asn Thr Asp
 75 80 85

ctc agt gaa gac tgt tta tat cta aat gta tgg att cca gca cct aaa 522
 Leu Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ile Pro Ala Pro Lys
 90 95 100

cca aaa aat gcc act gta ttg ata tgg att tat ggt ggt ggt ttt caa 570
 Pro Lys Asn Ala Thr Val Leu Ile Trp Ile Tyr Gly Gly Gly Phe Gln
 105 110 115

act gga aca tca tct tta cat gtt tat gat ggc aag ttt ctg gct cgg 618
 Thr Gly Thr Ser Ser Leu His Val Tyr Asp Gly Lys Phe Leu Ala Arg
 120 125 130 135

gtt gaa aga gtt att gta gtg tca atg aac tat agg gtg ggt gcc cta 666

Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	Asn	Tyr	Arg	Val	Gly	Ala	Leu		
				140					145					150			
gga	ttc	tta	gct	ttg	cca	gga	aat	cct	gag	gct	cca	ggg	aac	atg	ggt	714	
Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	Glu	Ala	Pro	Gly	Asn	Met	Gly		
			155					160					165				
tta	ttt	gat	caa	cag	ttg	gct	ctt	cag	tgg	gtt	caa	aaa	aat	ata	gca	762	
Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	Trp	Val	Gln	Lys	Asn	Ile	Ala		
		170						175				180					
gcc	ttt	ggt	gga	aat	cct	aaa	agt	gta	act	ctc	ttt	gga	gaa	agt	gca	810	
Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	Thr	Leu	Phe	Gly	Glu	Ser	Ala		
	185					190					195						
gga	gca	gct	tca	gtt	agc	ctg	cat	ttg	ctt	tct	cct	gga	agc	cat	tca	858	
Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	Leu	Ser	Pro	Gly	Ser	His	Ser		
200					205					210					215		
ttg	ttc	acc	aga	gcc	att	ctg	caa	agt	gga	tcc	ttt	aat	gct	cct	tgg	906	
Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	Gly	Ser	Phe	Asn	Ala	Pro	Trp		
			220						225					230			
gcg	gta	aca	tct	ctt	tat	gaa	gct	agg	aac	aga	acg	ttg	aac	tta	gct	954	
Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	Asn	Arg	Thr	Leu	Asn	Leu	Ala		
			235					240					245				
aaa	ttg	act	ggt	tgc	tct	aga	gag	aat	gag	act	gaa	ata	atc	aag	tgt	1002	
Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	Glu	Thr	Glu	Ile	Ile	Lys	Cys		
	250						255					260					
ctt	aga	aat	aaa	gat	ccc	caa	gaa	att	ctt	ctg	aat	gaa	gca	ttt	gtt	1050	
Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	Leu	Leu	Asn	Glu	Ala	Phe	Val		
	265					270					275						
gtc	ccc	tat	ggg	act	cag	ttg	tca	gta	aac	ttt	ggt	ccg	acc	gtg	gat	1098	
Val	Pro	Tyr	Gly	Thr	Gln	Leu	Ser	Val	Asn	Phe	Gly	Pro	Thr	Val	Asp		
280					285					290					295		
ggt	gat	ttt	ctc	act	gac	atg	cca	gac	ata	tta	ctt	gaa	ctt	gga	caa	1146	
Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	Ile	Leu	Leu	Glu	Leu	Gly	Gln		
				300					305					310			
ttt	aaa	aaa	acc	cag	att	ttg	gtg	ggt	gtt	aat	aaa	gat	gaa	ggg	aca	1194	
Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	Val	Asn	Lys	Asp	Glu	Gly	Thr		
			315					320					325				
gct	ttt	tta	gtc	tat	ggt	gct	cct	ggc	ttc	agc	aaa	gat	aac	aat	agt	1242	
Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	Phe	Ser	Lys	Asp	Asn	Asn	Ser		
		330					335					340					
atc	ata	act	aga	aaa	gaa	ttt	cag	gaa	ggt	tta	aaa	ata	ttt	ttt	cca	1290	
Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	Gly	Leu	Lys	Ile	Phe	Phe	Pro		

345	350	355	
gga gtg agt gag ttt gga aag gaa tcc atc ctt ttt cat tac aca gac			1338
Gly Val Ser Glu Phe	Gly Lys Glu Ser Ile	Leu Phe His Tyr Thr Asp	
360	365	370	375
tgg gta gat gat cag aga cct gaa aac tac cgt gag gcc ttg ggt gat			1386
Trp Val Asp Asp	Gln Arg Pro Glu Asn Tyr Arg	Glu Ala Leu Gly Asp	
	380	385	390
gtt gtt ggg gat tat aat ttc ata tgc cct gcc ttg gag ttc acc aag			1434
Val Val Gly Asp Tyr Asn Phe Ile Cys	Pro Ala Leu Glu Phe Thr Lys		
	395	400	405
aag ttc tca gaa tgg gga aat aat gcc ttt ttc tac tat ttt gaa cac			1482
Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe Phe Tyr Tyr Phe Glu His			
	410	415	420
cga tcc tcc aaa ctt ccg tgg cca gaa tgg atg gga gtg atg cat ggc			1530
Arg Ser Ser Lys Leu Pro Trp Pro Glu Trp Met	Gly Val Met His Gly		
	425	430	435
tat gaa att gaa ttt gtc ttt ggt tta cct ctg gaa aga aga gat aat			1578
Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro Leu Glu Arg Arg Asp Asn			
	440	445	450
tac aca aaa gcc gag gaa att ttg agt aga tcc ata gtg aaa cgg tgg			1626
Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg Ser Ile Val Lys Arg Trp			
	460	465	470
gca aat ttt gca aaa tat ggg aat cca aat gag act cag aac aat agc			1674
Ala Asn Phe Ala Lys Tyr Gly Asn Pro Asn Glu Thr Gln Asn Asn Ser			
	475	480	485
aca agc tgg cct gtc ttc aaa agc act gaa caa aaa tat cta acc ttg			1722
Thr Ser Trp Pro Val Phe Lys Ser Thr Glu Gln Lys Tyr Leu Thr Leu			
	490	495	500
aat aca gag tca aca aga ata atg acg aaa cta cgt gct caa caa tgt			1770
Asn Thr Glu Ser Thr Arg Ile Met Thr Lys Leu Arg Ala Gln Gln Cys			
	505	510	515
cga ttc tgg aca tca ttt ttt cca aaa gtc ttg gaa atg aca gga aat			1818
Arg Phe Trp Thr Ser Phe Phe Pro Lys Val Leu Glu Met Thr Gly Asn			
	520	525	530
att gat gaa gca gaa tgg gag tgg aaa gca gga ttc cat cgc tgg aac			1866
Ile Asp Glu Ala Glu Trp Glu Trp Lys Ala Gly Phe His Arg Trp Asn			
	540	545	550
aat tac atg atg gac tgg aaa aat caa ttt aac gat tac act agc aag			1914
Asn Tyr Met Met Asp Trp Lys Asn Gln Phe Asn Asp Tyr Thr Ser Lys			
	555	560	565

aaa gaa agt tgt gtg ggt ctc taattaatag atttaccctt tatagaacat 1965
Lys Glu Ser Cys Val Gly Leu
570

attttccttt agatcaaggc aaaaatatca ggagcttttt tacacaccta ctaaaaaagt 2025
tattatgtag ctgaaacaaa aatgccagaa ggataatatt gattcctcac atctttaact 2085
tagtatttta cctagcattt caaaacccaa atggctagaa catgtttaat taaatttcac 2145
aatataaagt tctacagtta attatgtgca tattaaaaca atggcctggt tcaatttctt 2205
tctttcctta ataaatttaa gttttttccc cccaaaatta tcagtgtctt gcttttagtc 2265
acgtgtattt tcattaccac tcgtaaaaag gtatcttttt taaatgaatt aaatattgaa 2325
acactgtaca ccatagttta caatattatg tttcctaatt aaaataagaa ttgaatgtca 2385
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<210> 6

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 6

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Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
	35						40				45				
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50					55					60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
	115						120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
	130					135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170					175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
	195						200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210						215				220				
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225					230					235					240

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Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn
      245                      250                      255
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile
      260                      265                      270
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Gln Leu Ser Val
      275                      280                      285
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp
      290                      295                      300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly
305                      310                      315                      320
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly
      325                      330                      335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu
      340                      345                      350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser
      355                      360                      365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
      370                      375                      380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
385                      390                      395                      400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
      405                      410                      415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
      420                      425                      430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
      435                      440                      445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
      450                      455                      460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465                      470                      475                      480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
      485                      490                      495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
      500                      505                      510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
      515                      520                      525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
      530                      535                      540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545                      550                      555                      560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
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<210> 7

<211> 2416

<212> DNA

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<221> CDS

<222> (214)...(1935)

<400> 7

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gaaatcaata	tgcatagcaa	agtcacaatc	atatgcatca	gatttctctt	ttggtttctt	180
ttgctctgca	tgcttattgg	gaagtcacat	act gaa gat	gac atc ata	att gca	234
			Glu Asp Asp	Ile Ile Ile	Ala	
			1		5	
aca aag aat	gga aaa gtc	aga ggg atg	aac ttg aca	gtt ttt ggt	ggc	282
Thr Lys Asn	Gly Lys Val	Arg Gly Met	Asn Leu Thr	Val Phe Gly	Gly	
	10	15		20		
acg gta aca	gcc ttt ctt	gga att ccc	tat gca cag	cca cct ctt	ggt	330
Thr Val Thr	Ala Phe Leu	Gly Ile Pro	Tyr Ala Gln	Pro Pro Leu	Gly	
	25	30	35			
aga ctt cga	ttc aaa aag	cca cag tct	ctg acc aag	tgg tct gat	att	378
Arg Leu Arg	Phe Lys Lys	Pro Gln Ser	Leu Thr Lys	Trp Ser Asp	Ile	
40	45		50		55	
tgg aat gcc	aca aaa tat	gca aat tct	tgc tgt cag	aac ata gat	caa	426
Trp Asn Ala	Thr Lys Tyr	Ala Asn Ser	Cys Cys Gln	Asn Ile Asp	Gln	
	60	65		70		
agt ttt cca	ggc ttc cat	gga tca gag	atg tgg aac	cca aac act	gac	474
Ser Phe Pro	Gly Phe His	Gly Ser Glu	Met Trp Asn	Pro Asn Thr	Asp	
	75	80		85		
ctc agt gaa	gac tgt tta	tat cta aat	gta tgg att	cca gca cct	aaa	522
Leu Ser Glu	Asp Cys Leu	Tyr Leu Asn	Val Trp Ile	Pro Ala Pro	Lys	
	90	95		100		
cca aaa aat	gcc act gta	ttg ata tgg	att tat ggt	ggt ggt ttt	caa	570
Pro Lys Asn	Ala Thr Val	Leu Ile Trp	Ile Tyr Gly	Gly Gly Phe	Gln	
105		110		115		
act gga aca	tca tct tta	cat gtt tat	gat ggc aag	ttt ctg gct	cgg	618
Thr Gly Thr	Ser Ser Leu	His Val Tyr	Asp Gly Lys	Phe Leu Ala	Arg	
120	125		130		135	
gtt gaa aga	gtt att gta	gtg tca atg	aac tat agg	gtg ggt gcc	cta	666
Val Glu Arg	Val Ile Val	Val Ser Met	Asn Tyr Arg	Val Gly Ala	Leu	
	140		145		150	
gga ttc tta	gct ttg cca	gga aat cct	gag gct cca	ggg aac atg	ggt	714
Gly Phe Leu	Ala Leu Pro	Gly Asn Pro	Glu Ala Pro	Gly Asn Met	Gly	
	155	160		165		
tta ttt gat	caa cag ttg	gct ctt cag	tgg gtt caa	aaa aat ata	gca	762
Leu Phe Asp	Gln Gln Leu	Ala Leu Gln	Trp Val Gln	Lys Asn Ile	Ala	
	170	175		180		

gcc ttt ggt gga aat cct aaa agt gta act ctc ttt gga gaa agt gca	810
Ala Phe Gly Gly Asn Pro Lys Ser Val Thr Leu Phe Gly Glu Ser Ala	
185 190 195	
gga gca gct tca gtt agc ctg cat ttg ctt tct cct gga agc cat tca	858
Gly Ala Ala Ser Val Ser Leu His Leu Leu Ser Pro Gly Ser His Ser	
200 205 210 215	
ttg ttc acc aga gcc att ctg caa agt gga tcc ttt aat gct cct tgg	906
Leu Phe Thr Arg Ala Ile Leu Gln Ser Gly Ser Phe Asn Ala Pro Trp	
220 225 230	
gcg gta aca tct ctt tat gaa gct agg aac aga acg ttg aac tta gct	954
Ala Val Thr Ser Leu Tyr Glu Ala Arg Asn Arg Thr Leu Asn Leu Ala	
235 240 245	
aaa ttg act ggt tgc tct aga gag aat gag act gaa ata atc aag tgt	1002
Lys Leu Thr Gly Cys Ser Arg Glu Asn Glu Thr Glu Ile Ile Lys Cys	
250 255 260	
ctt aga aat aaa gat ccc caa gaa att ctt ctg aat gaa gca ttt gtt	1050
Leu Arg Asn Lys Asp Pro Gln Glu Ile Leu Leu Asn Glu Ala Phe Val	
265 270 275	
gtc ccc tat ggg act tcg ttg tca gta aac ttt ggt ccg acc gtg gat	1098
Val Pro Tyr Gly Thr Ser Leu Ser Val Asn Phe Gly Pro Thr Val Asp	
280 285 290 295	
ggg gat ttt ctc act gac atg cca gac ata tta ctt gaa ctt gga caa	1146
Gly Asp Phe Leu Thr Asp Met Pro Asp Ile Leu Leu Glu Leu Gly Gln	
300 305 310	
ttt aaa aaa acc cag att ttg gtg ggt gtt aat aaa gat gaa ggg aca	1194
Phe Lys Lys Thr Gln Ile Leu Val Gly Val Asn Lys Asp Glu Gly Thr	
315 320 325	
gct ttt tta gtc tat ggt gct cct ggc ttc agc aaa gat aac aat agt	1242
Ala Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp Asn Asn Ser	
330 335 340	
atc ata act aga aaa gaa ttt cag gaa ggt tta aaa ata ttt ttt cca	1290
Ile Ile Thr Arg Lys Glu Phe Gln Glu Gly Leu Lys Ile Phe Phe Pro	
345 350 355	
gga gtg agt gag ttt gga aag gaa tcc atc ctt ttt cat tac aca gac	1338
Gly Val Ser Glu Phe Gly Lys Glu Ser Ile Leu Phe His Tyr Thr Asp	
360 365 370 375	
tgg gta gat gat cag aga cct gaa aac tac cgt gag gcc ttg ggt gat	1386
Trp Val Asp Asp Gln Arg Pro Glu Asn Tyr Arg Glu Ala Leu Gly Asp	
380 385 390	

gtt gtt ggg gat tat aat ttc ata tgc cct gcc ttg gag ttc acc aag	1434
Val Val Gly Asp Tyr Asn Phe Ile Cys Pro Ala Leu Glu Phe Thr Lys	
395 400 405	
aag ttc tca gaa tgg gga aat aat gcc ttt ttc tac tat ttt gaa cac	1482
Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe Phe Tyr Tyr Phe Glu His	
410 415 420	
cga tcc tcc aaa ctt ccg tgg cca gaa tgg atg gga gtg atg cat ggc	1530
Arg Ser Ser Lys Leu Pro Trp Pro Glu Trp Met Gly Val Met His Gly	
425 430 435	
tat gaa att gaa ttt gtc ttt ggt tta cct ctg gaa aga aga gat aat	1578
Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro Leu Glu Arg Arg Asp Asn	
440 445 450 455	
tac aca aaa gcc gag gaa att ttg agt aga tcc ata gtg aaa cgg tgg	1626
Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg Ser Ile Val Lys Arg Trp	
460 465 470	
gca aat ttt gca aaa tat ggg aat cca aat gag act cag aac aat agc	1674
Ala Asn Phe Ala Lys Tyr Gly Asn Pro Asn Glu Thr Gln Asn Asn Ser	
475 480 485	
aca agc tgg cct gtc ttc aaa agc act gaa caa aaa tat cta acc ttg	1722
Thr Ser Trp Pro Val Phe Lys Ser Thr Glu Gln Lys Tyr Leu Thr Leu	
490 495 500	
aat aca gag tca aca aga ata atg acg aaa cta cgt gct caa caa tgt	1770
Asn Thr Glu Ser Thr Arg Ile Met Thr Lys Leu Arg Ala Gln Gln Cys	
505 510 515	
cga ttc tgg aca tca ttt ttt cca aaa gtc ttg gaa atg aca gga aat	1818
Arg Phe Trp Thr Ser Phe Phe Pro Lys Val Leu Glu Met Thr Gly Asn	
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att gat gaa gca gaa tgg gag tgg aaa gca gga ttc cat cgc tgg aac	1866
Ile Asp Glu Ala Glu Trp Glu Trp Lys Ala Gly Phe His Arg Trp Asn	
540 545 550	
aat tac atg atg gac tgg aaa aat caa ttt aac gat tac act agc aag	1914
Asn Tyr Met Met Asp Trp Lys Asn Gln Phe Asn Asp Tyr Thr Ser Lys	
555 560 565	
aaa gaa agt tgt gtg ggt ctc taattaatag atttaccctt tatagaacat	1965
Lys Glu Ser Cys Val Gly Leu	
570	
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tattatgtag ctgaaacaaa aatgccagaa ggataatatt gattcctcac atctttaact	2085
tagtattttta cctagcattt caaaacccaa atggctagaa catgtttaat taaatttcac	2145
aatataaagt tctacagtta attatgtgca tattaaaaca atggcctggt tcaatttctt	2205
tctttcctta ataaatttaa gttttttccc cccaaaatta tcagtgtctt gcttttagtc	2265

acgtgtatatt tcattaccac tcgtaaaaag gtatcttttt taaatgaatt aaatattgaa 2325
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<210> 8

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 8

Glu	Asp	Asp	Ile	Ile	Ile	Ala	Thr	Lys	Asn	Gly	Lys	Val	Arg	Gly	Met	1	5	10	15
Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro	20	25	30	
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser	35	40	45	
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	50	55	60	
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	65	70	75	80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	85	90	95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	100	105	110	
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	115	120	125	
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	130	135	140	
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	145	150	155	160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	165	170	175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	180	185	190	
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	195	200	205	
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	210	215	220	
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	225	230	235	240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	245	250	255	
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270	
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Ser	Leu	Ser	Val	275	280	285	
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	290	295	300	
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	305	310	315	320

Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
		355					360					365			
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385					390					395					400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala
				405					410					415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu
			420					425					430		
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu
	435					440					445				
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser
	450					455					460				
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro
465					470					475					480
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr
				485					490					495	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr
			500					505					510		
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys
		515					520					525			
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys
	530					535					540				
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln
545					550					555					560
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu		
				565					570						

<210> 9

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 9

Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	Met	Trp
1				5					10				15	

<210> 10

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 10

Leu Ile Trp Ile Tyr Gly Gly Gly Phe Gln Thr Gly
1 5 10

<210> 11

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 11

Leu Phe Gly Glu Ser Ala Gly Ala
1 5

<210> 12

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 12

Ser Gly Ser Phe Asn Ala Pro Trp Ala Val Thr
1 5 10

<210> 13

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 13

Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val Asn
1 5 10

<210> 14

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 14

Thr Ala Phe Leu Val Tyr

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5

<210> 15

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Butyrylcholinesterase variant

<400> 15

Pro Trp Pro Glu Trp Met Gly Val Met His Gly Tyr Glu Ile

1

5

10

<210> 16

<211> 2416

<212> DNA

<213> Homo sapiens

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gaaatcaata	tgcatagcaa	agtcacaatc	atatgcatca	gatttctctt	ttggtttctt	180
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aatggaaaag	tcagagggat	gaacttgaca	gtttttgggt	gcacggtaac	agcctttctt	300
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ctggaaagaa	gagataatta	cacaaaagcc	gaggaaattt	tgagtagatc	catagtgaag	1620
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<210> 17

<211> 574

<212> PRT

<213> Homo sapiens

<400> 17

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      20             25             30
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser
      35             40             45
Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser
      50             55             60
Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu
65             70             75             80
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn
      85             90             95
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp
      100            105            110
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr
      115            120            125
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met
      130            135            140
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro
145            150            155            160
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln
      165            170            175
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val
      180            185            190
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu
      195            200            205
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser
      210            215            220
Gly Ser Phe Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg
225            230            235            240
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn
      245            250            255
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile

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			260					265				270			
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val
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Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
	290					295					300				
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
			325						330					335	
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
		340						345					350		
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser
	355					360					365				
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn
	370					375					380				
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys
385					390					395					400
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ser	Glu	Trp	Gly	Asn	Asn	Ala
			405					410						415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu
		420						425					430		
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu
	435					440					445				
Pro	Leu	Glu	Arg	Arg	Asp	Asn	Tyr	Thr	Lys	Ala	Glu	Glu	Ile	Leu	Ser
	450					455					460				
Arg	Ser	Ile	Val	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro
465					470					475					480
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr
			485						490					495	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr
		500						505					510		
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys
	515						520					525			
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys
	530					535					540				
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln
545					550					555					560
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu		
			565					570							

<210> 18
 <211> 574
 <212> PRT
 <213> Homo sapiens

<400> 18
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 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser
 35 40 45

Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser
50 55 60
Cys Cys Gln Asn Ile Gly Gln Ser Phe Pro Gly Phe His Gly Ser Glu
65 70 75 80
Met Trp Asn Pro Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn
85 90 95
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp
100 105 110
Ile Tyr Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr
115 120 125
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met
130 135 140
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro
145 150 155 160
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln
165 170 175
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val
180 185 190
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu
195 200 205
Leu Ser Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser
210 215 220
Gly Ser Phe Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg
225 230 235 240
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn
245 250 255
Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile
260 265 270
Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val
275 280 285
Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp
290 295 300
Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly
305 310 315 320
Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly
325 330 335
Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu
340 345 350
Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser
355 360 365
Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
370 375 380
Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
385 390 395 400
Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
405 410 415
Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
420 425 430
Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
435 440 445
Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
450 455 460
Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro

465		470		475		480									
Asn	Glu	Thr	Gln	Asn	Asn	Ser	Thr	Ser	Trp	Pro	Val	Phe	Lys	Ser	Thr
				485					490					495	
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Thr	Arg	Ile	Met	Thr
			500					505					510		
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Ser	Phe	Phe	Pro	Lys
		515					520					525			
Val	Leu	Glu	Met	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Trp	Glu	Trp	Lys
	530					535					540				
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln
545					550					555					560
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Val	Gly	Leu		
				565					570						

<210> 19
 <211> 574
 <212> PRT
 <213> Homo sapiens

<400> 19

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Asn	Leu	Thr	Val	Phe	Gly	Gly	Thr	Val	Thr	Ala	Phe	Leu	Gly	Ile	Pro
			20					25					30		
Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Ser
	35					40					45				
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
	50				55						60				
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu
65				70						75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr
	115						120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
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145				150					155						160
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
			165					170						175	
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180				185						190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu
	195						200					205			
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
	210					215					220				
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg
225				230					235						240
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn
				245					250					255	

Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile
 260 265 270
 Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val
 275 280 285
 Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp
 290 295 300
 Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly
 305 310 315 320
 Val Asn Lys Asp Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly
 325 330 335
 Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu
 340 345 350
 Gly Leu Lys Ile Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser
 355 360 365
 Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn
 370 375 380
 Tyr Arg Glu Ala Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys
 385 390 395 400
 Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala
 405 410 415
 Phe Phe Tyr Tyr Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu
 420 425 430
 Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu
 435 440 445
 Pro Leu Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser
 450 455 460
 Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
 465 470 475 480
 Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
 485 490 495
 Val Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
 500 505 510
 Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
 515 520 525
 Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys
 530 535 540
 Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
 545 550 555 560
 Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
 565 570

<210> 20
 <211> 574
 <212> PRT
 <213> Homo sapiens

<400> 20
 Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met
 1 5 10 15
 Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
 20 25 30
 Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser

		35					40					45				
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser	
	50					55					60					
Cys	Cys	Gln	Asn	Ile	Asp	Gln	Ser	Phe	Pro	Gly	Phe	His	Gly	Ser	Glu	
65					70					75					80	
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	
				85					90					95		
Val	Trp	Ile	Pro	Ala	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Leu	Ile	Trp	
			100						105				110			
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	His	Val	Tyr	
		115						120				125				
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met	
	130					135					140					
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro	
145					150					155					160	
Glu	Ala	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln	
				165					170					175		
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val	
			180					185					190			
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	Leu	His	Leu	
		195					200					205				
Leu	Ser	Pro	Gly	Ser	His	Ser	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser	
	210					215					220					
Gly	Ser	Phe	Asn	Ala	Pro	Trp	Ala	Val	Thr	Ser	Leu	Tyr	Glu	Ala	Arg	
225					230					235					240	
Asn	Arg	Thr	Leu	Asn	Leu	Ala	Lys	Leu	Thr	Gly	Cys	Ser	Arg	Glu	Asn	
				245					250					255		
Glu	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
Leu	Leu	Asn	Glu	Ala	Phe	Val	Val	Pro	Tyr	Gly	Thr	Pro	Leu	Ser	Val	
		275					280					285				
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
Ile	Leu	Leu	Glu	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Lys	Glu	Ser	
		355					360					365				
Ile	Leu	Phe	His	Tyr	Thr	Asp	Trp	Val	Asp	Asp	Gln	Arg	Pro	Glu	Asn	
	370					375					380					
Tyr	Arg	Glu	Ala	Leu	Gly	Asp	Val	Val	Gly	Asp	Tyr	Asn	Phe	Ile	Cys	
385					390					395						

Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro
465 470 475 480
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr
485 490 495
Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr
500 505 510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys
515 520 525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Thr Glu Trp Glu Trp Lys
530 535 540
Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln
545 550 555 560
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
565 570

<210> 21

<211> 574

<212> PRT

<213> Equus caballus

<400> 21

Glu Glu Asp Ile Ile Ile Thr Thr Lys Asn Gly Lys Val Arg Gly Met
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Asn Leu Pro Val Leu Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
20 25 30
Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser
35 40 45
Leu Thr Lys Trp Ser Asn Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser
50 55 60
Cys Tyr Gln Asn Thr Asp Gln Ser Phe Pro Gly Phe Leu Gly Ser Glu
65 70 75 80
Met Trp Asn Pro Asn Thr Glu Leu Ser Glu Asp Cys Leu Tyr Leu Asn
85 90 95
Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Met Ile Trp
100 105 110
Ile Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu Pro Val Tyr
115 120 125
Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met
130 135 140
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Leu Ser Glu Asn Pro
145 150 155 160
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln
165 170 175
Trp Val Gln Lys Asn Ile Ala Ala Phe Gly Gly Asn Pro Arg Ser Val
180 185 190
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu
195 200 205
Leu Ser Pro Arg Ser Gln Pro Leu Phe Thr Arg Ala Ile Leu Gln Ser
210 215 220
Gly Ser Ser Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg
225 230 235 240
Asn Arg Thr Leu Thr Leu Ala Lys Arg Met Gly Cys Ser Arg Asp Asn

				245					250					255		
Glu	Thr	Glu	Met	Ile	Lys	Cys	Leu	Arg	Asp	Lys	Asp	Pro	Gln	Glu	Ile	
			260					265					270			
Leu	Leu	Asn	Glu	Val	Phe	Val	Val	Pro	Tyr	Asp	Thr	Leu	Leu	Ser	Val	
		275					280					285				
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp	
	290					295					300					
Thr	Leu	Leu	Gln	Leu	Gly	Gln	Phe	Lys	Arg	Thr	Gln	Ile	Leu	Val	Gly	
305					310					315					320	
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	
				325					330					335		
Phe	Ser	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu	
			340					345					350			
Gly	Leu	Lys	Ile	Phe	Phe	Pro	Arg	Val	Ser	Glu	Phe	Gly	Arg	Glu	Ser	
		355					360					365				
Ile	Leu	Phe	His	Tyr	Met	Asp	Trp	Leu	Asp	Asp	Gln	Arg	Ala	Glu	Asn	
	370					375					380					
Tyr	Arg	Glu	Ala	Leu	Asp	Asp	Val	Val	Gly	Asp	Tyr	Asn	Ile	Ile	Cys	
385					390					395					400	
Pro	Ala	Leu	Glu	Phe	Thr	Arg	Lys	Phe	Ser	Glu	Leu	Gly	Asn	Asp	Ala	
				405					410					415		
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Thr	Lys	Leu	Pro	Trp	Pro	Glu	
			420					425					430			
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	
		435				440						445				
Pro	Leu	Glu	Arg	Arg	Val	Asn	Tyr	Thr	Arg	Ala	Glu	Glu	Ile	Leu	Ser	
	450					455					460					
Arg	Ser	Ile	Met	Lys	Arg	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	Asn	Pro	
465					470					475					480	
Asn	Gly	Thr	Gln	Asn	Asn	Ser	Thr	Arg	Trp	Pro	Val	Phe	Lys	Ser	Thr	
				485					490					495		
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Ser	Pro	Lys	Val	Tyr	Thr	
			500					505					510			
Lys	Leu	Arg	Ala	Gln	Gln	Cys	Arg	Phe	Trp	Thr	Leu	Phe	Phe	Pro	Lys	
		515					520					525				
Val	Leu	Glu	Leu	Thr	Gly	Asn	Ile	Asp	Glu	Ala	Glu	Arg	Glu	Trp	Lys	
	530					535					540					
Ala	Gly	Phe	His	Arg	Trp	Asn	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	
545					550					555					560	
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Ser	Cys	Ser	Asp	Phe			
				565					570							

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<210> 22
<211> 574
<212> PRT
<213> Felis catus
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<400> 22
Glu Glu Asp Ile Ile Ile Thr Thr Lys Asn Gly Lys Val Arg Gly Met
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Asn Leu Pro Val Leu Asp Gly Thr Val Thr Ala Phe Leu Gly Ile Pro
20 25 30

Tyr	Ala	Gln	Pro	Pro	Leu	Gly	Arg	Leu	Arg	Phe	Lys	Lys	Pro	Gln	Phe
		35					40					45			
Leu	Thr	Lys	Trp	Ser	Asp	Ile	Trp	Asn	Ala	Thr	Lys	Tyr	Ala	Asn	Ser
		50				55					60				
Cys	Tyr	Gln	Asn	Ala	Asp	Gln	Ser	Phe	Pro	Gly	Phe	Pro	Gly	Ser	Glu
65					70					75					80
Met	Trp	Asn	Pro	Asn	Thr	Asp	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
				85					90					95	
Val	Trp	Ile	Pro	Thr	Pro	Lys	Pro	Lys	Asn	Ala	Thr	Val	Met	Ile	Trp
			100					105					110		
Ile	Tyr	Gly	Gly	Gly	Phe	Gln	Thr	Gly	Thr	Ser	Ser	Leu	Pro	Val	Tyr
		115					120					125			
Asp	Gly	Lys	Phe	Leu	Ala	Arg	Val	Glu	Arg	Val	Ile	Val	Val	Ser	Met
		130				135					140				
Asn	Tyr	Arg	Val	Gly	Ala	Leu	Gly	Phe	Leu	Ala	Leu	Pro	Gly	Asn	Pro
145					150					155					160
Glu	Val	Pro	Gly	Asn	Met	Gly	Leu	Phe	Asp	Gln	Gln	Leu	Ala	Leu	Gln
				165					170						175
Trp	Val	Gln	Lys	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asn	Pro	Lys	Ser	Val
			180					185					190		
Thr	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Gly	Ser	Val	Ser	Leu	His	Leu
		195					200					205			
Leu	Ser	Pro	Arg	Ser	Gln	Pro	Leu	Phe	Thr	Arg	Ala	Ile	Leu	Gln	Ser
		210				215					220				
Gly	Ser	Ser	Asn	Ala	Pro	Trp	Ala	Val	Met	Ser	Leu	Asp	Glu	Ala	Lys
225					230					235					240
Asn	Arg	Thr	Leu	Thr	Leu	Ala	Lys	Phe	Ile	Gly	Cys	Ser	Lys	Glu	Asn
				245					250					255	
Asp	Thr	Glu	Ile	Ile	Lys	Cys	Leu	Arg	Asn	Lys	Asp	Pro	Gln	Glu	Ile
		260						265					270		
Leu	Leu	Asn	Glu	Leu	Leu	Val	Val	Pro	Ser	Asp	Thr	Leu	Leu	Ser	Val
		275					280					285			
Asn	Phe	Gly	Pro	Val	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	Asp
		290				295					300				
Thr	Leu	Leu	Gln	Leu	Gly	Gln	Phe	Lys	Lys	Thr	Gln	Ile	Leu	Val	Gly
305					310					315					320
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly
				325					330					335	
Phe	Ser	Lys	Asp	Asn	Asp	Ser	Ile	Ile	Thr	Arg	Lys	Glu	Phe	Gln	Glu
			340					345					350		
Gly	Leu	Lys	Ile	Tyr	Phe	Pro	Gly	Val	Ser	Glu	Phe	Gly	Arg	Glu	Ala
		355					360					365			
Ile	Leu	Phe	Tyr	Tyr	Val	Asp	Leu	Leu	Asp	Asp	Gln	Arg	Ala	Glu	Lys
		370				375					380				
Tyr	Arg	Glu	Ala	Leu	Asp	Asp	Val	Leu	Gly	Asp	Tyr	Asn	Ile	Ile	Cys
385					390					395					400
Pro	Ala	Leu	Glu	Phe	Thr	Thr	Lys	Phe	Ser	Glu	Leu	Gly	Asn	Asn	Ala
				405					410					415	
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Gln	Leu	Pro	Trp	Pro	Glu
			420					425					430		
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu
		435					440					445			
Pro	Leu	Glu	Arg	Arg	Val	Asn	Tyr	Thr	Arg	Ala	Glu	Glu	Ile	Leu	Ser

450		455		460
Arg Ser Ile Met Asn Tyr Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro				
465		470		475
Asn Gly Thr Gln Asn Asn Ser Thr Arg Trp Pro Ala Phe Arg Ser Thr				
	485		490	495
Asp Gln Lys Tyr Leu Thr Leu Asn Ala Glu Ser Pro Lys Val Tyr Thr				
	500		505	510
Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Leu Phe Phe Pro Lys				
	515		520	525
Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu Arg Glu Trp Arg				
	530		535	540
Ala Gly Phe Tyr Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln				
545		550		555
Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser Cys Ala Gly Leu				
	565		570	

<210> 23
 <211> 574
 <212> PRT
 <213> Rattus sp.

<400> 23

Glu Glu Asp Val Ile Ile Thr Thr Lys Thr Gly Arg Val Arg Gly Leu				
1	5	10	15	
Ser Met Pro Ile Leu Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro				
	20	25	30	
Tyr Ala Gln Pro Pro Leu Gly Ser Leu Arg Phe Lys Lys Pro Gln Pro				
	35	40	45	
Leu Asn Lys Trp Pro Asp Val Tyr Asn Ala Thr Lys Tyr Ala Asn Ser				
	50	55	60	
Cys Tyr Gln Asn Ile Asp Gln Ala Phe Pro Gly Phe Gln Gly Ser Glu				
65	70	75	80	
Met Trp Asn Pro Asn Thr Asn Leu Ser Glu Asp Cys Leu Tyr Leu Asn				
	85	90	95	
Val Trp Ile Pro Val Pro Lys Pro Lys Asn Ala Thr Val Met Val Trp				
	100	105	110	
Val Tyr Gly Gly Gly Phe Gln Thr Gly Thr Ser Ser Leu Pro Val Tyr				
	115	120	125	
Asp Gly Lys Phe Leu Thr Arg Val Glu Arg Val Ile Val Val Ser Met				
	130	135	140	
Asn Tyr Arg Val Gly Ala Leu Gly Phe Leu Ala Phe Pro Gly Asn Ser				
145	150	155	160	
Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln				
	165	170	175	
Trp Ile Gln Arg Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val				
	180	185	190	
Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu				
	195	200	205	
Leu Cys Pro Gln Ser Tyr Pro Leu Phe Thr Arg Ala Ile Leu Glu Ser				
	210	215	220	
Gly Ser Ser Asn Ala Pro Trp Ala Val Lys His Pro Glu Glu Ala Arg				
225	230	235	240	

Asn	Arg	Thr	Leu	Thr	Leu	Ala	Lys	Phe	Ile	Gly	Cys	Ser	Lys	Glu	Asn	245	250	255
Glu	Lys	Glu	Ile	Ile	Thr	Cys	Leu	Arg	Ser	Lys	Asp	Pro	Gln	Glu	Ile	260	265	270
Leu	Leu	Asn	Glu	Lys	Leu	Val	Leu	Pro	Ser	Asp	Ser	Ile	Arg	Ser	Ile	275	280	285
Asn	Phe	Gly	Pro	Thr	Val	Asp	Gly	Asp	Phe	Leu	Thr	Asp	Met	Pro	His	290	295	300
Thr	Leu	Leu	Gln	Leu	Gly	Lys	Val	Lys	Thr	Ala	Gln	Ile	Leu	Val	Gly	305	310	315
Val	Asn	Lys	Asp	Glu	Gly	Thr	Ala	Phe	Leu	Val	Tyr	Gly	Ala	Pro	Gly	325	330	335
Phe	Ser	Lys	Asp	Asn	Asp	Ser	Leu	Ile	Thr	Arg	Arg	Glu	Phe	Gln	Glu	340	345	350
Gly	Leu	Asn	Met	Tyr	Phe	Pro	Gly	Val	Ser	Ser	Leu	Gly	Lys	Glu	Ala	355	360	365
Ile	Leu	Phe	Tyr	Tyr	Val	Asp	Trp	Leu	Gly	Asp	Gln	Thr	Pro	Glu	Val	370	375	380
Tyr	Arg	Glu	Ala	Phe	Asp	Asp	Ile	Ile	Gly	Asp	Tyr	Asn	Ile	Ile	Cys	385	390	395
Pro	Ala	Leu	Glu	Phe	Thr	Lys	Lys	Phe	Ala	Glu	Leu	Glu	Ile	Asn	Ala	405	410	415
Phe	Phe	Tyr	Tyr	Phe	Glu	His	Arg	Ser	Ser	Lys	Leu	Pro	Trp	Pro	Glu	420	425	430
Trp	Met	Gly	Val	Met	His	Gly	Tyr	Glu	Ile	Glu	Phe	Val	Phe	Gly	Leu	435	440	445
Pro	Leu	Glu	Arg	Arg	Val	Asn	Tyr	Thr	Arg	Ala	Glu	Glu	Ile	Phe	Ser	450	455	460
Arg	Ser	Ile	Met	Lys	Thr	Trp	Ala	Asn	Phe	Ala	Lys	Tyr	Gly	His	Pro	465	470	475
Asn	Gly	Thr	Gln	Gly	Asn	Ser	Thr	Val	Trp	Pro	Val	Phe	Thr	Ser	Thr	485	490	495
Glu	Gln	Lys	Tyr	Leu	Thr	Leu	Asn	Thr	Glu	Lys	Ser	Lys	Ile	Asn	Ser	500	505	510
Lys	Leu	Arg	Ala	Pro	Gln	Cys	Gln	Phe	Trp	Arg	Leu	Phe	Phe	Pro	Lys	515	520	525
Val	Leu	Glu	Ile	Thr	Gly	Asp	Ile	Asp	Glu	Arg	Glu	Gln	Glu	Trp	Lys	530	535	540
Ala	Gly	Phe	His	Arg	Trp	Ser	Asn	Tyr	Met	Met	Asp	Trp	Lys	Asn	Gln	545	550	555
Phe	Asn	Asp	Tyr	Thr	Ser	Lys	Lys	Glu	Thr	Cys	Thr	Asp	Leu			565	570	

<210> 24

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> human butyrylcholinesterase variant

<400> 24

gaagttccta ttctctagaa agtataggaa cttc 34

<210> 25
<211> 15
<212> DNA
<213> Homo sapiens

<400> 25
actcctttgt cagta 15

<210> 26
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> human butyrylcholinesterase variant

<400> 26
actcctttgg gtgta 15

<210> 27
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> human butyrylcholinesterase variant

<400> 27
actcagttgt cagta 15

<210> 28
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> human butyrylcholinesterase variant

<400> 28
acttcgttgt cagta 15

<210> 29
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer


<400> 29
atagactaaa aaccatgtcc cttcatc 27

<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 30
taatacgact cactataggg

20

 <210> 31
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 31
atttaggtga cacttatag

19
